

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Lal, Preeti
Shah, Purvi
Corley, Neil C.
- (ii) TITLE OF THE INVENTION: HUMAN PREPRONEUROTENSIN/NEUROMEDIN N
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0450 US
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-845-4166
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: PITUNOT03
(B) CLONE: 1760566
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Met Met Ala Gly Met Lys Ile Gln Leu Val Cys Met Leu Leu Leu Ala
 1      5      10      15
Phe Ser Ser Trp Ser Leu Cys Ser Asp Ser Glu Glu Glu Met Lys Ala
 20      25      30
Leu Glu Ala Asp Phe Leu Thr Asn Met His Thr Ser Lys Ile Ser Lys
 35      40      45
Ala His Val Pro Ser Trp Lys Met Thr Leu Leu Asn Val Cys Ser Leu
 50      55      60
Val Asn Asn Leu Asn Ser Pro Ala Glu Glu Thr Gly Glu Val His Glu
 65      70      75      80
Glu Glu Leu Val Ala Arg Arg Lys Leu Pro Thr Ala Leu Asp Gly Phe
 85      90      95
Ser Leu Glu Ala Met Leu Thr Ile Tyr Gln Leu His Lys Ile Cys His
 100      105      110
Ser Arg Ala Phe Gln His Trp Glu Leu Ile Gln Glu Asp Ile Leu Asp
 115      120      125
Thr Gly Asn Asp Lys Asn Gly Lys Glu Glu Val Ile Lys Arg Lys Ile
 130      135      140
Pro Tyr Ile Leu Lys Arg Gln Leu Tyr Glu Asn Lys Pro Arg Arg Pro
 145      150      155      160
Tyr Ile Leu Lys Arg Asp Ser Tyr Tyr Tyr
      165      170

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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NNTCAAAGCC AGCTGAAGGA AAGAGGAAGT GCTAGAGAGA GCCCCCTTCA GTGTGCTTCT 60
GACTTTTACG GACTTGGCTT GTTAGAAGGC TGAAGATGA TGGCAGGAAT GAAAATCCAG 120
CTTGTATGCA TGCTACTCCT GGCTTTCAGC TCCTGGAGTC TGTGCTCAGA TTCAGAAGAG 180
GAAATGAAAG CATTAGAAGC AGATTTCTTG ACCAATATGC ATACATCAAA GATTAGTAAA 240
GCACATGTTT CCTCTTGGA GATGACTCTG CTAAATGTTT GCAGTCTTGT AAATAATTTG 300
AACAGCCCAG CTGAGGAAAC AGGAGAAAGT CATGAAGAGG AGCTTGTTGC AAGAAGGAAA 360
CTTCCTACTG CTTTAGATGG CTTTAGCTTG GAAGCAATGT TGACAATATA CCAGCTCCAC 420
AAAATCTGTC ACAGCAGGGC TTTTCAACAC TGGGAGTTAA TCCAGGAAGA TATTCTTGAT 480
ACTGGAATG ACAAAAATGG AAAGGAAGAA GTCATAAAGA GAAAAATTCC TTATATTCTG 540
AAACGGCAGC TGTATGAGAA TAAACCCAGA AGACCCTACA TACTCAAAAG AGATTCTTAC 600
TATTACTGAG AGAATAAATC ATTTATTTAC ATGTGATTGT GATTCATCAT CCCTTAATTA 660
AATATCAAAT TATATTTGTG TGAAAATGTG ACAAACACAC TTATCTGTCT CTTCTACAAT 720
TGTGGTTTAT TGAATGTGAT TTTTCTGCAC TAATATAAAT TAGACTAAGT GTTTTCAAAT 780
AAATCTAAAT CTTCAGCATG ATGTGTTGTG TATAATTGGA GTAGATATTA ATTAAGTCAC 840
CTGTATAATG TTTTGTAATT TTGCAAAACA TATCTTGAGT TGTTTAAACA GTCAAAATGT 900
TTGATATTTT ATACCAGCTT ATGAGCTCAA AGTACTACAG CAAAGCCTAG CCTGCATATC 960
ATTCACCCAA AACAAAGTAA TAGCGCCTCT TTTATTATTT TGAAGTGAATG TTTTATGGAA 1020
TTGAAAGAAA CATACGTTCT TTTCAAGACT TCCTCATGAA TCTCTCAATT ATAGGAAAAG 1080
TTATTGTGAT AAAATAGGAA CAGCTGAAAG ATTGATTAAT GAACTATTGT TATTACTTCC 1140
TATTTTAATG AATGACATTG AACTGGATTT TTTGACCTGT TAATGGACTT GGTAGCTATT 1200
AGAAGGACAC TTGACCTCCA ATAGAAAAAA ATAAAAGAAA TAAAAAGAAG TATAAAAGTA 1260
ATAAAATAAA ATCAGAAGAG AAAAAGAAAA AGAAAAGTAA AAAGAGGGGG GACACACCAT 1320
AAGAACCAAT ACCCGGGAAT TTTCGGAGCG A
1351

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 163424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Met Ala Gly Met Lys Ile Gln Leu Val Cys Met Ile Leu Leu Ala Phe
 1          5          10          15
Ser Ser Trp Ser Leu Cys Ser Asp Ser Glu Glu Glu Met Lys Ala Leu
 20          25          30
Glu Thr Asp Leu Leu Thr Asn Met His Thr Ser Lys Ile Ser Lys Ala
 35          40          45
Ser Val Pro Ser Trp Lys Met Ser Leu Leu Asn Val Cys Ser Leu Ile
 50          55          60
Asn Asn Leu Asn Ser Gln Ala Glu Glu Thr Gly Glu Phe His Glu Glu
 65          70          75          80
Glu Leu Ile Thr Arg Arg Lys Phe Pro Ala Ala Leu Asp Gly Phe Ser
 85          90          95
Leu Glu Ala Met Leu Thr Ile Tyr Gln Leu Gln Lys Ile Cys His Ser
100          105          110
Arg Ala Phe Gln His Trp Glu Leu Ile Gln Glu Asp Ile Leu Asp Ala
115          120          125
Gly Asn Asp Lys Asn Glu Lys Glu Glu Val Ile Lys Arg Lys Ile Pro
130          135          140
Tyr Ile Leu Lys Arg Gln Leu Tyr Glu Asn Lys Pro Arg Arg Pro Tyr
145          150          155          160
Ile Leu Lys Arg Gly Ser Tyr Tyr Tyr
165

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 92546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Ile Gly Met Asn Leu Gln Leu Val Cys Leu Thr Leu Leu Ala Phe
 1          5          10          15
Ser Ser Trp Ser Leu Cys Ser Asp Ser Glu Glu Asp Val Arg Ala Leu
 20          25          30
Glu Ala Asp Leu Leu Thr Asn Met His Ala Ser Lys Val Ser Lys Gly
 35          40          45
Ser Pro Pro Ser Trp Lys Met Thr Leu Leu Asn Val Cys Ser Leu Ile
 50          55          60
Asn Asn Leu Asn Ser Ala Ala Glu Glu Ala Gly Glu Met Arg Asp Asp
 65          70          75          80
Asp Leu Val Ala Lys Arg Lys Leu Pro Leu Val Leu Asp Asp Phe Ser
 85          90          95

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Leu	Glu	Ala	Leu	Leu	Thr	Val	Phe	Gln	Leu	Gln	Lys	Ile	Cys	Arg	Ser
			100					105					110		
Arg	Ala	Phe	Gln	His	Trp	Glu	Ile	Ile	Gln	Glu	Asp	Ile	Leu	Asp	His
		115					120					125			
Gly	Asn	Glu	Lys	Thr	Glu	Lys	Glu	Glu	Val	Ile	Lys	Arg	Lys	Ile	Pro
	130					135					140				
Tyr	Ile	Leu	Lys	Arg	Gln	Leu	Tyr	Glu	Asn	Lys	Pro	Arg	Arg	Pro	Tyr
145					150					155					160
Ile	Leu	Lys	Arg	Ala	Ser	Tyr	Tyr	Tyr							
				165											